

[illegible][illegible]

FIGURE 2

GCGGAAGTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCCCCGGCTGGCCTAGG
CAGGCAGCCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCTGCTCAGCTTCCTGGGCATGGTGGGCA
CGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCT
ACCTGAAAGGGCTCTGGATGGAGTGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGC
TGGCGCTGCCCCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCG
CCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTGCCATCCTCG
GCGGCACCCTCTTCATCCTGGCCGGCCCTCCTGTGCATGGTGGCCGTCTCCTGGACCACCAACGACGTGGTGCAGA
ACTTCTACAACCCGCTGCTGCCCAGCGGCATGAAGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCT
CGTCCCTCTCGCTCATTGGTGGCACCCCTGCTTTGCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGG
CCCCGCCCAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATC
GGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTGTGAGTCCCCACAGCCTGCT
TCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGGTTCAGCACAAAGTTTAC
TTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGG
AAATAAGAGGAGGAGAAAGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATTATAT
ATATTTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGTTGGTTTGTG
ATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 3

CAGGACCAGGTCTTCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG
 ATCTGCTGACGCTGGGCCCCGCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG
 GAGAAGCCACTGCCCACCGCCTTCTGCTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCTGACTGGCTGAAGCTG
 CGCATGATCCGTTCTGAGGTGCTCCGCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTG
 TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCCTCCAGTTCCTGGACCAGGCAGTGGCCAC
 GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCCACCTGGTGGAGGTCCAGCATGAGCGC
 GGCGCTCCGGAGGCCAGACTTTCCACTCCTTGCTCACAGCCTCCCTGCCGCCCCGCCGAGACAGCACAGAGGCA
 CCCAAACCAAAGAGCAGCCCAGAGCAGCCCATAGGCCAGGGCCGGATTTCGGGTGGGGACCCAGCTCCGGGTGCTG
 GGCCCTGAGGACGACCTGGCTGGCATGTTCTCCTCCAGATTTTCCCGCTCAGCCCGGACCCTCGGTGGCAGAGCTCC
 AGTCCCCGCCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGGCAGGAGCTGGCCCCGCTGCTCCAGGGCAGCCCC
 GAGGTGCCGGGCATCACGGTGCGTGTCTGCAGGCCCTCGCCACCCTGCTCAGCTCCCCACACGGCGGTGCCCTG
 GTGATGTCCATGCACCGTAGCCACTTCTGGCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGTG
 CCACAGGACACCGGCTTCTCCTCGCTCTTCTGAAGGTGCTCCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC
 GTGGAGGGCGGGCCCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCCTCAGCCGGGCGCAGGCTCAGTGAT
 GTGCGAGGGGGGCTCCTGCGCCTGGCCGAGGCCCTGGCCTTCCGTGAGGACCTGGAGGTGGTTCAGCTCCACCGTC
 CGTGCCGTTCATCGCCACCCTGAGGTCTGGGGAGCAGTGCGAGCTGGAGCCGGACCTGATCAGCAAAGTCTCCTCAG
 GGGCTGATCGAGGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTCTGCCACTGCGGATGCTGCC
 TCCCCGTTCACAGCCTGTAAGCCCGTTGTGGTGAGCTCCCTGCTGCTGCAGGAGGAGGAGCCCCCTGGCTGGG
 GGGAAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCTCGTCAGGCCTCCTAGTGGACTGG
 CTGGAATGCTGGACCCCCAGGTGGTTCAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGGAGGAAG
 GGCAAAGGTGAGGCCCAGGTGCCCTCGTTCCGTCCCTACCTCCTGACCCTCTTCACGCATCAGTCCAGCTGGCCC
 AACTGACACAGTGCATCCGAGTCTGCTGGGCAAGAGCCGGGAACAGAGGTTTCGACCCCTCTGCCTCTCTGGAC
 TTCCTCTGGGCCTGCATCCATGTTCTCTGCATCTGGCAGGGGCGGGACCAGCGCACCCCGCAGAAGCGGCGGGAG
 GAGCTGGTGCTGCGGGTCCAGGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG
 AGCCAGGACGGGGACACAGCCGCTGCAGCCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG
 GACGATGAGAGTGTGAGGAAGGTGACGGAGCACCTGTGAGGCTGCATCCAGCAGTGGGGAGACAGCGTGTGGGA
 AGGCGCTGCCGAGACCTTCTCCTGCAGCTCTACCTACAGCGGCCCGGAGCTGCGGGTGCCCGTGCCTGAGGTCTTA
 CTGCACAGCGAAGGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGACGGACTCATCCACCGCTTCATCACGCTCCTT
 GCGGACACCAAGGACTCCCCGGGCGTTGGAGAACCAGGGGGCGGATGCCAGCATGGCCTGCCGGAAGCTGGCGGTG
 GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCCTGCACGGCCGACCCACCTCAACTTC
 CAGGAGTTCGGCGAGCAGAACCACCTGAGCTGCTTCTGTCAGCTGCTGGGCTGCTGGAGCTGCTGCAGCCGCAC
 GTGTTCCGCGAGCGAGCACAGGGGGCGCTGTGGGACTGCCTTCTGTCTTTCATCCGCTGCTGCTGAATTACAGG
 AAGTCTCTCCGCCATCTGGCTGCCTTCATCAACAAGTTTGTGAGTTTCATCCATAAGTACATTACCTACAATGCC
 CCAGCAGCCATCTCCTTCTGTCAGAAGCAGCCGACCCGCTCCACGACCTGTCTTCGACAACAGTGACCTGGTG
 ATGCTGAAATCCCTCCTTGAGGGCTCAGCCTGCCAGCAGGGACGACAGGACCGACCGAGGCCTGGACGAAGAG
 GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGCCCTGGTCAAGCTCTCCTGTTACCCCTCTGACCGCGGCCGAG
 ATGGCCCCCTACATGAAACGGCTTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
 GAGATGTCCCGGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG
 GAGTGTTCGCGCAACCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTC
 CTGCCCACGTTTCATGTACTGCCTGGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTGAG
 TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGCCCTTCTGGTGGGCATGTACGGCCAGATG
 GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGTGAGCCTGTGGCAGCCGA
 CCCCCCTCCAAGCCCCGGCCCGTCCCGTCCCCGGGGATCCTCGAGGCCAAAGCCCAGGAAGCGTGGGCGTTGCTGG
 TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGCAGGCCAGGAGCAATACTCCGAGCCCTGGGGTGG
 CTCCGGGCGGCCGCTGGCATCAGGGGCCGTCCAGCAAGCCCTCATTCACCTTCTGGGCCACAGCCCTGCCGCGG
 AGCGGCGGATCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAACTGTCAA

FIGURE 5

MTLRPSLLPLHLLLLLLLLLAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHIHYTGSLVDGRIID
TSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGFPPSPADAVVQYDVELIALIRANYWL
KLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVSKKKLKEEKRNKSKKK

Signal peptide.

amino acids 1-25

Transmembrane domain.

amino acids 155-174

N-glycosylation site.

amino acids 196-200

N-myristoylation site.

amino acids 95-101

Amidation site.

amino acids 119-123

FKBP-type peptidyl-prolyl cis-trans isomerase signature 1.

amino acids 62-78, 87-124, 128-142

FIGURE 6

MASTAVQLLGFLLSFLGMVGTLLITLPHWRRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQCQIYRSLLALPQ
DLQAARALMVISCLLSGIACACAVIGMKCTRCAGKTPAKTTFAILGGTLFILAGLLCMVAVSWTTNDVVQNFYNP
LLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQDEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSV
TSATHSGYRLNDYV

Signal sequence.

amino acids 1-21

Transmembrane domains.

amino acids 78-98, 116-136, 162-182

N-myristoylation sites.

amino acids 17-22, 20-25, 60-65, 92-97, 101-106, 178-183

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 85-95, 87-97

PMP-22/EMP/MP20/Claudin family.

amino acids 4-181

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FIGURE 7

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRMIRSEVLRLVDAAL
 QDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNYMAHLVEVQHERGASGGQTFHSLITAS
 LPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLGPEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQ
 ELARVVQGSPEVPGITVRVLQALATLLSSPHGGALVMSMHRSHFLACPLLRLCQYQRCVPQDTGFSSFLKVL
 QMLQWLDSPGVEGGPLRAQLRMLASQASAGRRLSDVRGGLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQCSV
 EPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASPPACKPVVVVSSLLIQEEEPLAGGKPGADGGSLEAVRL
 GPSSGLLDVWLEMLDPEVVSSCPDLQLRLLESRRKGKGQAQVPSFRPYLLTLETHQSSWPTLHQCIRVLLGKSRE
 QRFDPASLDLFWACIHVPRIWQGRDQRTQPQKRREELVLRVQGPESISVELILAEAETRSQDGDAAACSLIQAR
 LPLLLSCCCGDDSVRKVTEHLSGCIQQWGDSVLGRRCRDLLLQLYLQRPVPEVLLHSEGAASSSVCKLD
 GLIHRFITLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPMAALLHGRTHLNFQEFQQNHLSCFLHV
 LGLELLQPHVFRSEHQGALWDCLLSFIRLLLNYRKSSRHAAAFINKFVQFIHKYITYNAPAAISFLQKHADPLH
 DLSFDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAGSLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVE
 DLLEVLSDIDEMSRRRPEILSFFSTNLQRLMSSAECCRNLAFLSLALRSMQNSPSIAAAFLPTFMYCLGSQDFEV
 VQTALRNLPEYALLCQEHAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

Signal peptide.

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449, 665-671,
 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 8

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIIITSKGGKGNANLEYKTGAF
SMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSC
MIENDIAKATGDIKVTESSEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYMLK

Signal peptide.

amino acids 1-28

Transmembrane domain.

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220, 220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

Immunoglobulin domain.

amino acids 49-132